

TABLE 1. Sample sizes for each locus and population used in this study. Mitochondrial loci (Control Region and cytochrome *b*) are haplotypic.

		BC	WA	OR	CA	Total
Microsatellites	uapi-23	24	102	38	31	195
	12a12	24	101	38	30	193
	12a22	24	104	39	31	198
	14b29	24	104	39	31	198
	uaa5-8	24	103	38	30	195
Sequences						
	Control Region 3'	24	10	21	21	76
	Control Region 5'	24	69	38	30	161
	Cytochrome <i>b</i>	24	11	21	18	74
	α - Enolase	24	11	21	18	74
Total Genotypes/Haplotypes		216	615	284	240	1,364

TABLE 2. Primers and PCR conditions for each locus. For those loci that are sequenced, different primer concentrations and annealing conditions are used during the sequencing procedure

Locus	PRIMERS ¹	Primer Concentration	MgCl ₂	Annealing	# Cycles	Multiplex
uapi-23	F: 6-FAM -CCGTGTTGAAATAGAACAGA R: TTTAGCTGGTGAAGTTAGTCAG	0.17µM	1.5mM	58°C	35	1
12a12	F: HEX-TCTACGATTCTATGATTCCACA R: GATCTCTACCACATTCTCCCTA	0.60µM	3.5mM	56°C	35	
12a22	F: 6-FAM -CAGTGTCAAGGAGAGG R: TAGGGCTTATGCCAGAGAGAC	0.10µM	1.5mM	54°C	31	2
14b29	F: TET-GTATTATGTCGGAAACTGTT R: TACCCCTATATACAACCCAAAG	0.28µM	1.5mM	54°C	31	2
uaa5-8	F: 6-FAM -CAGTTCTTAAGTCGTGCCAG R: CACTTAGTCCAAACCTAACCC	0.11µM	1.5mM	58°C	35	1
cytochrome b ²	L: CCATCCAAACATCTCAGCATGATGAAA H: GCDCCTCAGAATGATAATTGTCCTCA	1.0µM	2.5 mM	5°C	30	
α - enolase	L: TGGACTTCAAATCCCCCGATGATCCCAGC H: CCAGGCACCCAGTCTACCTGGTCAAA	1.0µM	2.5 mM	6°C	30	
control region 5'	L: CCATTAATAACACACAGACATAACC H: CGGGTGAGATGGTGTATAGCCG	0.80µM	1.5mM	54°C	31	
control region 3'	L: CAATAAACCCCTCCAGTGCACCG H: CGTTCGAGTATATGAACGTAGGTTG	0.80µM	1.5mM	50°C	30	

Each PCR cocktail also included 10x buffer solution (10mM Tris HCL (pH 9.0 at 25°C), 50mM KCL, 0.1% TritonX-100), 200 µM dNTPs, and 0.03 units of Taq (Promega)

¹ F (forward), R (reverse), L (light strand), H (heavy strand) primers. 6-FAM, HEX, and TET are phosphoramidite reagent dyes that are incorporated on the 5' end of the forward primers of each microsatellite and emit fluorescence when excited by a laser. These dyes are used with the ABI 377 semi-automated sequencer (Perkin-Elmer Biosystems)

² The cytochrome b primers are L14841 and H15149 from Koeter et al. (1989)

TABLE 3. Genetic diversity indices. The multi-population probability is that associated with heterozygote deficiency with all populations pooled. Probabilities in bold typeface are significant at the $p \leq 0.05$ level

	BC	WA	OR	CA
uapi-23				
# alleles	10	15	10	12
Heterozygosity - Expected	0.84	0.81	0.66	0.75
Heterozygosity - Observed	0.79	0.76	0.63	0.81
Probability (<i>multi-pop: p=0.01</i>)	0.80	0.03	0.10	0.54
Null allele Frequency (r)	0.03	0.03	0.02	-0.03
12a12				
# alleles	5	5	5	5
Heterozygosity - Expected	0.70	0.75	0.65	0.70
Heterozygosity - Observed	0.50	0.36	0.24	0.30
Probability (<i>multi-pop: p=0.00</i>)	0.04	0.00	0.00	0.00
Null allele Frequency (r)	0.12	0.22	0.25	0.24
12a22				
# alleles	4	4	4	4
Heterozygosity - Expected	0.45	0.31	0.29	0.26
Heterozygosity - Observed	0.17	0.20	0.21	0.16
Probability (<i>multi-pop: p=0.00</i>)	0.00	0.00	0.00	0.01
Null allele Frequency (r)	0.19	0.08	0.06	0.08
14b29				
# alleles	10	15	9	10
Heterozygosity - Expected	0.69	0.79	0.68	0.71
Heterozygosity - Observed	0.71	0.79	0.64	0.52
Probability (<i>multi-pop: p=0.11</i>)	0.75	0.62	0.34	0.00
Null allele Frequency (r)	-0.01	0.00	0.02	0.11
uaa5-8				
# alleles	6	6	5	5
Heterozygosity - Expected	0.66	0.70	0.57	0.68
Heterozygosity - Observed	0.71	0.72	0.50	0.53
Probability (<i>multi-pop: p=0.12</i>)	0.41	0.39	0.52	0.38
Null allele Frequency (r)	-0.03	-0.01	0.04	0.09
Average All Loci				
# alleles	7.0	9.0	6.6	7.2
Heterozygosity - Expected	0.67	0.67	0.57	0.62
Heterozygosity - Observed	0.58	0.57	0.44	0.46
Probability	0.00	0.00	0.00	0.01
F_{IS}	0.14	0.16	0.23	0.26

TABLE 4. Allele sizes and frequencies for each locus and population. The probability column indicates those allele frequencies that are significantly different among some or all populations (see text)

uapi-23	WA	CA	OR	BC	p ≤ 0.05
161	0.010	0.000	0.000	0.000	•
167	0.005	0.017	0.015	0.000	•
169	0.382	0.397	0.455	0.333	•
171	0.069	0.069	0.030	0.083	•
175	0.025	0.086	0.030	0.042	•
177	0.059	0.069	0.076	0.063	•
179	0.044	0.000	0.015	0.063	wa > ca
181	0.157	0.155	0.061	0.167	•
183	0.069	0.052	0.076	0.083	•
185	0.088	0.017	0.152	0.125	•
187	0.044	0.069	0.091	0.021	•
189	0.005	0.000	0.000	0.000	•
191	0.034	0.034	0.000	0.000	wa > or, bc
193	0.005	0.000	0.000	0.000	•
195	0.000	0.000	0.000	0.021	•
197	0.000	0.017	0.000	0.000	•
207	0.005	0.000	0.000	0.000	•
209	0.000	0.017	0.000	0.000	•

12a12	WA	CA	OR	BC	p ≤ 0.05
100	0.317	0.304	0.318	0.313	•
108	0.282	0.125	0.152	0.438	bc > ca, or
110	0.198	0.214	0.152	0.146	•
112	0.178	0.321	0.333	0.063	ca, or > bc
114	0.025	0.036	0.045	0.042	•

12a22	WA	CA	OR	BC	p ≤ 0.05
137	0.034	0.054	0.029	0.042	•
139	0.043	0.089	0.074	0.083	•
141	0.822	0.839	0.809	0.729	•
143	0.101	0.018	0.088	0.146	•

TABLE 4 (con't)

14b29	WA	CA	OR	BC	p ≤ 0.05
129	0.394	0.431	0.412	0.521	•
133	0.005	0.000	0.000	0.000	•
134	0.010	0.069	0.000	0.021	•
137	0.024	0.017	0.000	0.021	wa > or
139	0.188	0.224	0.191	0.208	•
141	0.106	0.069	0.074	0.042	•
143	0.096	0.069	0.103	0.000	wa, or > bc
145	0.019	0.017	0.044	0.000	•
147	0.034	0.052	0.059	0.042	•
149	0.019	0.017	0.015	0.042	•
151	0.053	0.034	0.015	0.063	•
153	0.024	0.000	0.000	0.000	wa > ca, or, bc
155	0.019	0.000	0.088	0.021	wa, or > ca
157	0.005	0.000	0.000	0.021	•
163	0.005	0.000	0.000	0.000	•

uaa5-8	WA	CA	OR	BC	p ≤ 0.05
106	0.034	0.054	0.000	0.021	•
108	0.126	0.161	0.091	0.083	•
110	0.374	0.357	0.424	0.396	•
112	0.039	0.000	0.030	0.042	•
116	0.374	0.357	0.394	0.438	•
118	0.053	0.071	0.061	0.021	•

TABLE 5. *F*-statistics for each locus, pooled across all populations. Values with asterisk are significantly greater than zero.

	uapi-23	12a12	12a22	14b29	uaa5-8	All Loci
θ (F_{ST})	0.000	0.018*	-0.005	-0.001	-0.008	0.001
f (F_{IS})	0.032	0.527*	0.397*	0.046	0.033	0.182*

TABLE 6. Results from four separate analyses of molecular variance (AMOVAs).

Analysis		Percentage of Variation		
# Loci ^a	Group	Among Group	Among Population ^b	Within Population
5	None		0.36	99.64
3	None	-	1.77	98.23
3	WA-OR CA-BC	-1.98	3.03	98.94
3	WA-BC OR-CA	2.26	0.18	97.56

^a The three loci analyses included uapi-23, 12a12, 14b29

^b For analyses with groups, among population variation equals variation between the two populations within each group.

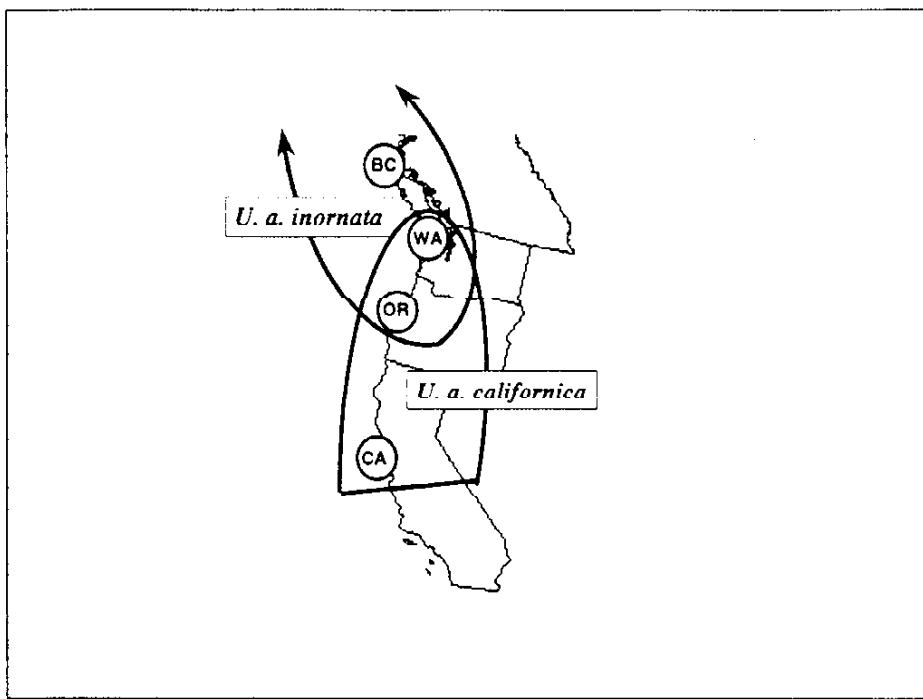


Figure 1. DNA samples were obtained from either tissue or blood from four localities. BC: Winter Harbour, British Columbia (north of Triangle Island). WA: Cape Flattery, Washington. OR: Newport, Oregon. CA: SE Farallon Island and Gulf of Farallones, California.

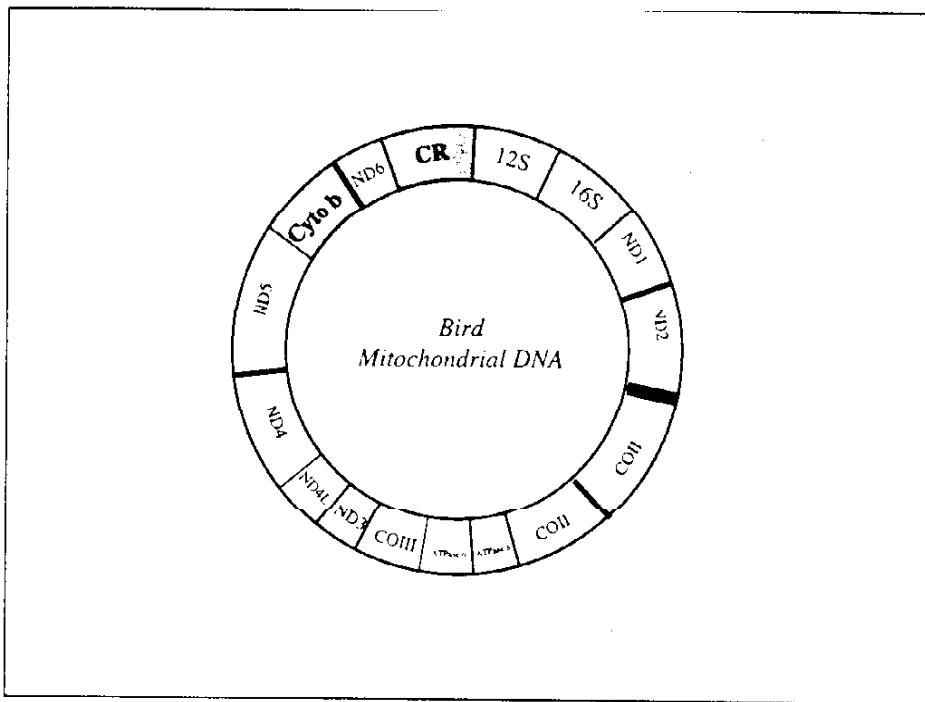


Figure 2. Schematic diagram of the gene content and order of the avian mitochondrial DNA (adapted from Quinn 1997). The relative location of the cytochrome *b* and control region loci are highlighted.

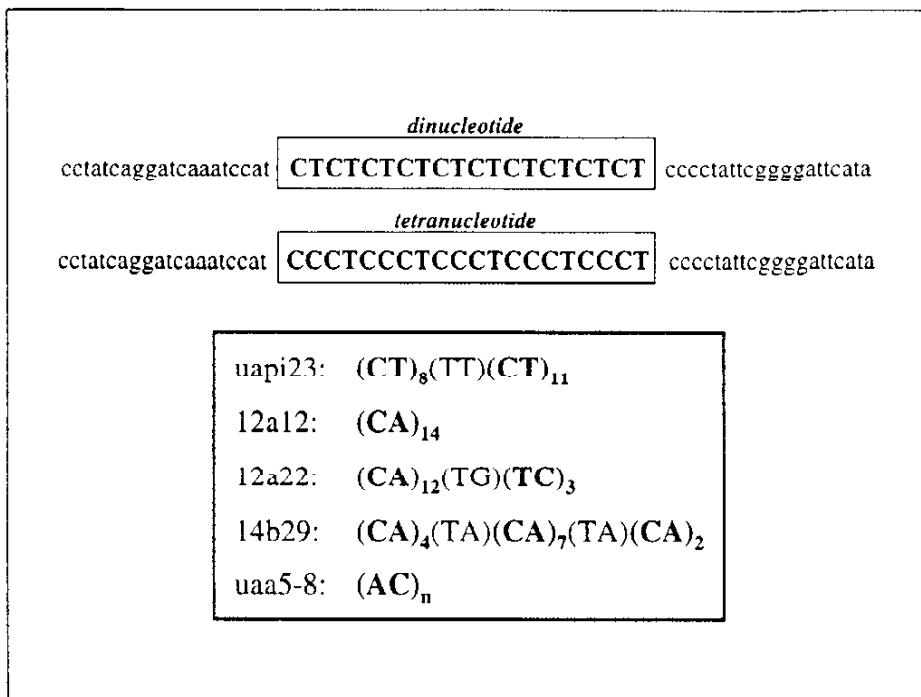
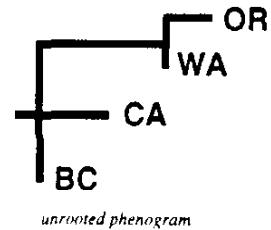


Figure 3. The top half of figure shows an example of a dinucleotide and a tetranucleotide microsatellite. The bottom half of the figure lists the microsatellite loci used in this analysis and the repeat motifs for the Common Murre individual from which the primers and protocols were derived.

$(\delta\mu)^2$	BC	CA	OR	WA
BC	0.000			
CA	0.140	0.000		
OR	1.449	1.462	0.000	
WA	0.930	1.083	0.090	0.000



F_{ST}	BC	CA	OR	WA
BC	0.000			
CA	0.059	0.000		
OR	0.050	-0.002	0.000	
WA	0.005	0.020	0.014	0.000

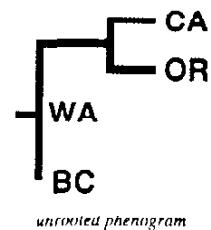


Figure 4. Genetic distance matrices $(\delta\mu)^2$ above and F_{ST} below, based on the three microsatellite loci with significant differences in allele frequencies (Table 4). Phenograms accompanying each matrix where generated using the Fitch program in *PhyliP* (Felsenstein 1993)

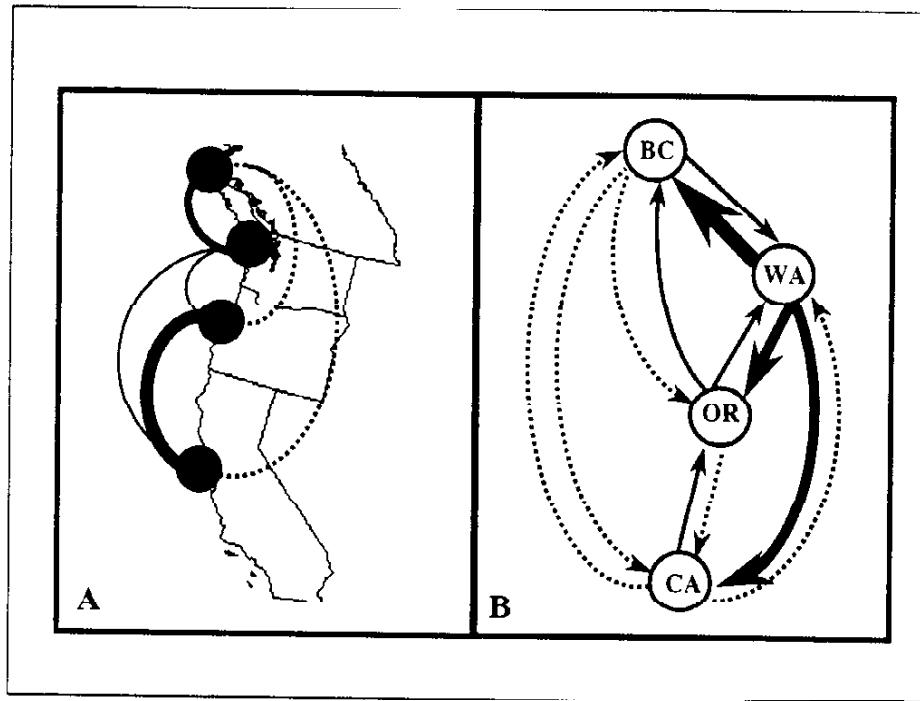


Figure 5. Patterns of gene flow among four Common Murre populations. (A) gene flow pattern based on F_{ST} values. Gene flow occurs in both directions along solid or dashed lines. Thickness of the line indicates relative amounts of gene flow, with the highest amount of gene flow occurring between Oregon and California and the lowest amount of gene flow between British Columbia and California and Oregon (dashed lines). (B) gene flow pattern based on maximum likelihood procedure (Reerli 1997). The direction of the arrow corresponds to the direction of movement of individuals. As with (A), the thickness of the line indicates relative amounts of gene flow. For example, most of the gene flow occurs as emigration from Washington, with minor gene flow from Oregon and British Columbia into Washington and from California and Oregon into Oregon and British Columbia, respectively. All other gene flow estimates are negligible.

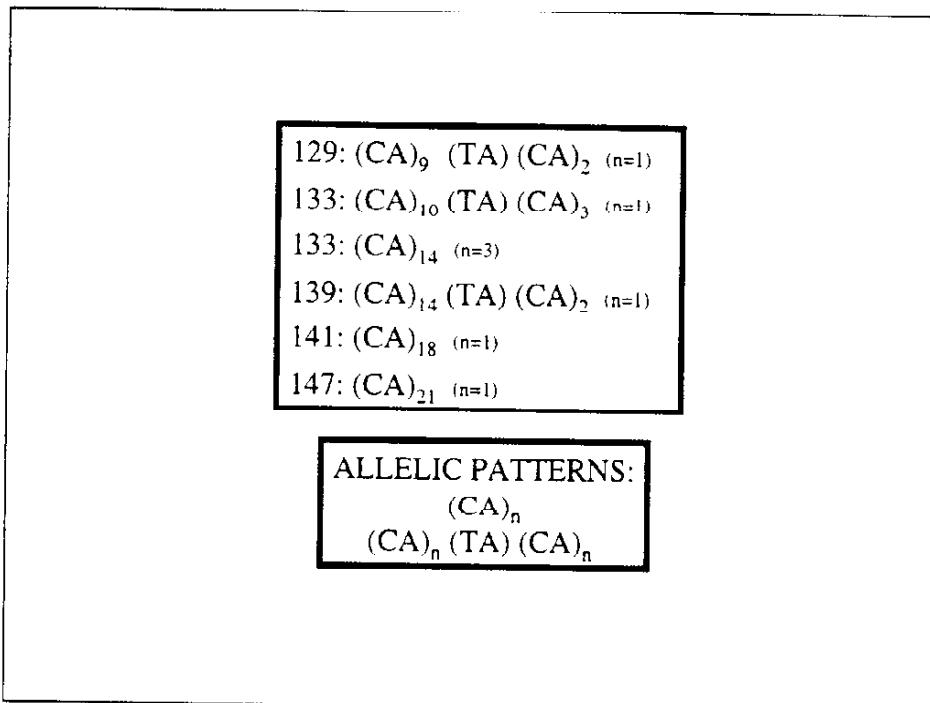


Figure 6. 14b29 microsatellite repeat motifs and allelic patterns for four individuals.

<u>JMB 1496:</u>	(CT) ₅ (TT) (CT) ₁₇ (CT) ₅ (TT) (CT) ₁₇
<u>JMB 1383:</u>	(CT) ₄ (CC) (CT) ₁₈ (CT) ₂₃
<u>kiw97-52:</u>	(CT) ₄ (CC) (CT) ₁₈ (CT) ₁₀ (TT) (CT) ₁₂ or (CT) ₄ (CC) (CT) ₅ (TT) (CT) ₁₂ (CT) ₂₃

ALLELIC PATTERNS:
(CT) _n
(CT) _n (TT) (CT) _n
(CT) _n (CC) (CT) _n
(CT) _n (CC) (CT) _n (TT) (CT) _n

Figure 7. uapi-23 microsatellite repeat motifs and allelic patterns for three individuals each homozygous for the 171 bp allele.

**TENYO MARU TRUSTEE COMMITTEE
RESOLUTION 1998-03
ADOPTED 25 MARCH 1998**

**TENYO MARU TRUSTEE COMMITTEE RESOLUTION AMENDING
RESOLUTION 96-06: APPROVAL OF 1996 PROJECT FUNDING**

Resolution: 1995-01 By-laws
 1995-03
 1995-04
 1995-05
 1996-06

Consent Decree: 4 Natural Resource Trustees
 13(f) Restoration Expenditure
 32 Restoration Plan
 Attachment A, 7 Expenditures from the Restoration
 Account
 Attachment B Memorandum of Agreement: Part 4 and 5

Adopted: April 21, 1997

The Tenyo Maru Natural Resource Trustees [the U.S. Department of the Interior, including the U.S. Fish and Wildlife Service (USFWS); the National Oceanic and Atmospheric Administration (NOAA) of the Department of Commerce; the State of Washington (State), and the Makah Indian Tribe] are preparing a Restoration Plan pursuant to a Consent Decree under United States et al. v. Maruha Corporation et al. (C94-1537, W.D. Wash., Dec. 23, 1994).

The Tenyo Maru Trustee Committee (Committee) hereby amends Resolution 96-06, adding authorized funding amounts to the approved 1996 projects, adding two projects, and revising the description of one project. The following table lists the approved 1996 projects with the approved dollar amounts:

1996 Project Name	1996 Authorized Funding
1) At Sea Distribution and Abundance of Marbled Murres and Common Murres-WA (WDFW)	\$42,217.00
1a) Cooperative Research Project with WDFW for Conducting Surveys of Seabird Utilization of Kelp Habitat (Makah Tribe)*	\$13,879.03
2) Replicate Aerial Census of Common Murres-OR (USFWS)♦	\$15,555.00
3) Replicate Aerial Census of Common Murres-WA (USFWS)	\$13,390.00
4) Common Murre Monitoring on Tatoosh Island (UW)	\$44,545.87
5) Population Genetic Analysis (WDFW)*	\$42,775.80

* Added project

♦ Description revised

Payment for these projects will be reviewed and authorized by the Committee as follows: 70% of the project costs may be authorized for disbursement upon receipt of the draft project report and appropriate invoices; remainder of the project costs will be authorized for disbursement upon review and approval of the final project report and receipt of final invoices.

By their signatures on the attached page, representatives of the Trustees hereby certify that this resolution was adopted in compliance with the decision-making procedures adopted by the Trustees, and that expenditure of the funds specified in the identified manner is consistent with the terms of the Consent Decree, the Memorandum of Agreement, and other applicable law.

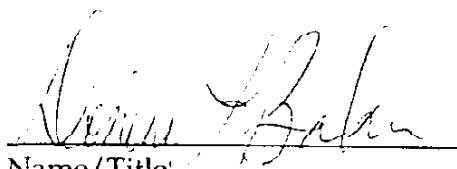
TENYO MARU TRUSTEE COMMITTEE RESOLUTION

RESOLUTION NUMBER 1998-03

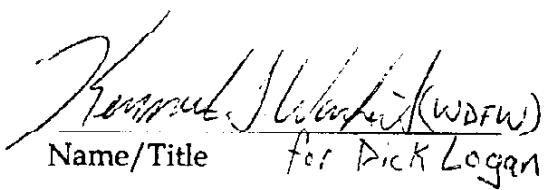
By unanimous consent, the Tenyo Maru Natural Resource Trustee Committee hereby adopts and approves the 1996 pilot projects and funding amounts.

Dated this 25th day of March, 1998.

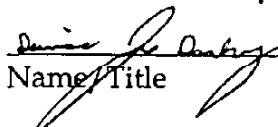
For the United States of America,
Department of Commerce/NOAA
Department of the Interior:


Name/Title

For the State of Washington,
Washington Department of Ecology:


Name/Title for Dick Logan

For the Makah Indian Tribe:


Name/Title

000233

FROM: STATE OF WASHINGTON
DEPARTMENT OF FISH AND
WILDLIFE
600 CAPITOL WAY NORTH
OLYMPIA, WA 98501-1091

INVOICE - VOUCHER
===== = ===== = =====
(FORM A-19)

TO: DENISE BAKER
TENYO MARU TRUSTEE COMMITTEE CHAIR
USFWS - WESTERN WASHINGTON OFFICE
510 DESMOND DRIVE SE; SUITE 102
LACEY, WA 98503

INVOICE NO. 47700-PT4100-9999
===== ===== =====
INVOICE DATE: 2000/01/26
===== ===== =====
CONTRACT NO: 01/18/00 E-MAIL
===== ===== =====
CONTACT PERSON: FRANK GESSWEIN
===== ===== =====
CONTACT PHONE NO. (360) 664-4992
===== ===== =====

CONTRACT TITLE: TENYO MARU GENETICS STUDY BN 97,99, & FY 00.

CONTRACT TERM: 07/01/95 - 12/31/99

BILLING PERIOD: 07/01/95 - 12/31/99

CONTRACT AMOUNT: \$41,503.24

BILLINGS TO DATE: \$41,603.24

CONTRACT BALANCE: \$0.00

PAST DUE AMOUNT: \$0.00

CURRENT MONTH BILLING AMOUNT: \$41,503.24

BILLING AMOUNT: \$41,503.24

TOTAL OVERHEAD 6,626.57

ACCOUNT CODE *FOR DEPARTMENT OF FISH AND WILDLIFE USE ONLY*

TRANS CODE	FUND	APPR INDEX	GL	PROJ	MAJOR GROUP	MAJO SRC	SUB SOURCE	PAYMENT AMOUNT
	001		1312		04	41	PT4100	34,876.67
	001		1312		04	40	IN4100	6,591.69
	001		1312		04	40	404100	34.88

***** IF NOT PAID BY: JUNE 30, 2000 TO BE RECORDED AS AN ACCRUAL TO: GL 1312 *****

Vendors Certificate. I hereby certify under penalty of perjury that the items & totals listed
herein are proper charges for materials, merchandise or services furnished to the State of
Washington, & that all goods furnished and/or services rendered have been provided without
discrimination on the grounds of race, creed, color, national origin, sex or age.

: Prepared by: _____ : DATE: _____ : Approved by: _____ : DATE: _____ :

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rev. 6/29/93 YELLOW COPY - RETURN WITH PAYMENT GOLDENROD COPY - ACCOUNTS RECEIVABLE FILE